



JOHNS HOPKINS
BLOOMBERG
SCHOOL of PUBLIC HEALTH

Department of Biostatistics

BIostatISTICS SEMINAR

Characterizing Genomic Variation from Both Known and Unknown Sources

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Abstract

One of the overarching goals of my lab is to develop and apply methods to characterize complex sources of variation in genomic data so that signals of interest may be accurately identified. We have developed methods that model high-dimensional data involving both known and unknown sources of systematic variation in settings applicable to data coming from microarrays, next-generation sequencing, and genome-wide association studies. We have also carried out experiments to directly dissect and better understand sources of variation in genomic data in terms of biological and technological factors. I will present several of our recent projects that seek to tackle these important challenges.

**The Johns Hopkins Bloomberg School of Public Health
Department of Biostatistics, Monday, October 7, 2013, 12:15-1:15pm
Room W4030, School of Public Health (Refreshments: 12:00)**

We request that lunch be eaten before or after seminar and not during the seminar

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